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OIPE

## RAW SEQUENCE LISTING

DATE: 03/12/2002

PATENT APPLICATION: US/10/084,843

TIME: 09:41:42

Input Set : N:\Crf3\RULE60\10084843.raw

Output Set: N:\CRF3\03122002\J084843.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Reed, Steven G.  
6 Skeiky, Yasir A.W.  
7 Dillon, Davin C.  
8 Campos-Neto, Antonio  
9 Houghton, Raymond  
10 Vedvick, Thomas S.  
11 Twardzik, Daniel R.  
12 Lodes, Michael J.  
13 Hendrickson, Ronald C.

ENTERED

15 (ii) TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY  
16 AND DIAGNOSIS OF TUBERCULOSIS

18 (iii) NUMBER OF SEQUENCES: 355

## 20 (iv) CORRESPONDENCE ADDRESS:

21 (A) ADDRESSEE: SEED and BERRY LLP  
22 (B) STREET: 6300 Columbia Center, 701 Fifth Avenue  
23 (C) CITY: Seattle  
24 (D) STATE: Washington  
25 (E) COUNTRY: USA  
26 (F) ZIP: 98104-7092

## 28 (v) COMPUTER READABLE FORM:

29 (A) MEDIUM TYPE: Floppy disk  
30 (B) COMPUTER: IBM PC compatible  
31 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
32 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## 34 (vi) CURRENT APPLICATION DATA:

C--> 35 (A) APPLICATION NUMBER: US/10/084,843  
C--> 36 (B) FILING DATE: 25-Feb-2002  
37 (C) CLASSIFICATION:

## 39 (vii) PRIOR APPLICATION DATA:

40 (A) APPLICATION NUMBER: US/09/072,967  
41 (B) FILING DATE: 05-MAY-1998

## 44 (viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Maki, David J.  
46 (B) REGISTRATION NUMBER: 31,392  
47 (C) REFERENCE/DOCKET NUMBER: 210121.411C9

## 49 (ix) TELECOMMUNICATION INFORMATION:

50 (A) TELEPHONE: (206) 622-4900  
51 (B) TELEFAX: (206) 682-6031

## 54 (2) INFORMATION FOR SEQ ID NO: 1:

## 56 (i) SEQUENCE CHARACTERISTICS:

57 (A) LENGTH: 766 base pairs

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Input Set : N:\Crf3\RULE60\10084843.raw

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58          (B) TYPE: nucleic acid
59          (C) STRANDEDNESS: single
60          (D) TOPOLOGY: linear
62      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64 CGAGGCACCG GTAGTTTGAA CCAAACGCAC AATCGACGGG CAAACGAACG GAAGAACACA      60
65 ACCATGAAGA TGGTGAAATC GATCGCCGCA GGTCTGACCG CCGCGGCTGC AATCGGCGCC      120
66 GCTGCGGCCG GTGTGACTTC GATCATGGCT GCGGCCCCCG TCGTATACCA GATGCAGCCG      180
67 GTCGTCTTCG GCGCGCCACT GCCGTTGGAC CCGGCATCCG CCCCTGACGT CCGACCGCC      240
68 GCCCAGTTGA CCAGCTGCT CAACAGCCTC GCCGATCCCA ACGTGTCGTT TCGGAACAAG      300
69 GGCAGTCTGG TCGAGGGCGG CATCGGGGGC ACCGAGGCGC GCATCGCCGA CCACAAGCTG      360
70 AAGAAGGCCG CCGAGCACGG GGATCTGCCG CTGTCGTTCA GCGTGACGAA CATCCAGCCG      420
71 GCGGCCGCCG GTTCGGCCAC CGCCGACGTT TCCGTCTCGG GTCCGAAGCT CTCGTCGCCG      480
72 GTCACGCAGA ACGTCACGTT CGTGAATCAA GGCGGCTGGA TGCTGTCACG CGCATCGGCG      540
73 ATGGAGTTGC TGCAGGCCGC AGGGNAACTG ATTGGCGGGC CGGNTTCAGC CCGCTGTTCA      600
74 GCTACGCCGC CGCCTGGTG ACGCGTCCAT GTCGAACACT CGCGCGTGTA GCACGGTGCG      660
75 GTNTGCGCAG GGNCGCACGC ACCGCCCCGT GCAAGCCGTC CTCGAGATAG GTGGTGNCTC      720
76 GNCACCAGNG ANCACCCCN NNTCGNCNNT TCTCGNTGNT GNATGA      766
78 (2) INFORMATION FOR SEQ ID NO: 2:
80      (i) SEQUENCE CHARACTERISTICS:
81          (A) LENGTH: 752 base pairs
82          (B) TYPE: nucleic acid
83          (C) STRANDEDNESS: single
84          (D) TOPOLOGY: linear
86      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
88 ATGCATCACC ATCACCATCA CGATGAAGTC ACGGTAGAGA CGACCTCCGT CTTCCGCGCA      60
89 GACTTCTCTA GCGAGCTGGA CGCTCCTGCG CAAGCGGGTA CGGAGAGCGC GGTCTCCGGG      120
90 GTGGAAGGGC TCCC GCCGGG CTCGGCGTTG CTGGTAGTCA AACGAGGCC CAAACCCGGG      180
91 TCCC GGTTCC TACTCGACCA AGCCATCACG TCGGCTGGTC GGCATCCCGA CAGCGACATA      240
92 TTTCTCGACG ACGTGACCGT GAGCCGTCGC CATGCTGAAT TCCGGTTGGA AAACAACGAA      300
93 TTCAATGTCG TCGATGTCGG GAGTCTCAAC GGCACCTACG TCAACCGCGA GCCCGTGGAT      360
94 TCGGCGGTGC TGGCGAACGG CGACGAGGTC CAGATCGGCA AGCTCCGGT GGTGTTCTTG      420
95 ACCGGACCCA AGCAAGGCGA GGATGACGGG AGTACCGGGG GCCCGTGAGC GCACCCGATA      480
96 GCCCCGCGCT GGCCGGGATG TCGATCGGGG CGGTCTCCG ACCTGCTACG ACCGGATTTT      540
97 CCCTGATGTC CACCATCTCC AAGATTCGAT TCTTGGGAGG CTTGAGGGTC NGGGTGACCC      600
98 CCCC GCGGGC CTCATT CNGG GGTNTCGGCN GGTTTCACCC CNTACCNACT GCCNCCCGGN      660
99 TTGCNAATTC NTTCTTCNCT GCCCNAAAAG GGACNNTAN CTTGCCGCTN GAAANGGTNA      720
100 TCCNGGGCCC NTCCTNGAAN CCCCNTCCCC CT      752
102 (2) INFORMATION FOR SEQ ID NO: 3:
104      (i) SEQUENCE CHARACTERISTICS:
105          (A) LENGTH: 813 base pairs
106          (B) TYPE: nucleic acid
107          (C) STRANDEDNESS: single
108          (D) TOPOLOGY: linear
110      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
112 CATATGCATC ACCATCACCA TCACACTTCT AACCGCCCAG CGGTCGGGG GCGTCGAGCA      60
113 CCACGCGACA CCGGGCCCGA TCGATCTGCT AGCTTGAGTC TGGTCAGGCA TCGTCGTCAG      120
114 CAGCGCGATG CCCTATGTTT GTCGTGCACT CAGATATCGC GGCAATCCAA TCTCCCGCCT      180
115 GCGGCCGGCG GTGCTGCAAA CTACTCCCGG AGGAATTTCTG ACGTGCGCAT CAAGATCTTC      240
116 ATGCTGGTCA CGGCTGTCGT TTTGCTCTGT TGTTCCGGTG TGGCCACGGC CGCGCCCAAG      300

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117 ACCTACTGCG AGGAGTTGAA AGGCACCGAT ACCGGCCAGG CGTGCCAGAT TCAAATGTCC 360
118 GACCCGGCCT ACAACATCAA CATCAGCCTG CCCAGTTACT ACCCCGACCA GAAGTCGCTG 420
119 GAAAATTACA TCGCCAGAC GCGCGACAAG TTCCTCAGCG CGGCCACATC GTCCACTCCA 480
120 CGCGAAGCCC CCTACGAATT GAATATCACC TCGGCCACAT ACCAGTCCGC GATACCGCCG 540
121 CGTGGTACGC AGGCCGTGGT GCTCAMGGTC TACCACAACG CCGGCGGCAC GCACCCAACG 600
122 ACCACGTACA AGGCCTTCGA TTGGGACCAG GCCTATCGCA AGCCAATCAC CTATGACACG 660
123 CTGTGGCAGG CTGACACCGA TCCGCTGCCA GTCGTCTTCC CCATTGTTGC AAGGTGAACT 720
124 GAGCAACGCA GACCGGGACA ACWGGTATCG ATAGCCGCCN AATGCCGGCT TGGAACCCNG 780
125 TGAAATTATC ACAACTTCGC AGTCACNAAA NAA 813
127 (2) INFORMATION FOR SEQ ID NO: 4:
129 (i) SEQUENCE CHARACTERISTICS:
130 (A) LENGTH: 447 base pairs
131 (B) TYPE: nucleic acid
132 (C) STRANDEDNESS: single
133 (D) TOPOLOGY: linear
135 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
137 CGGTATGAAC ACGGCCGCGT CCGATAACTT CCAGCTGTCC CAGGGTGGGC AGGGATTTCGC 60
138 CATTCCGATC GGGCAGGCGA TGGCGATCGC GGGCCAGATC CGATCGGGTG GGGGGTCACC 120
139 CACCGTTCAT ATCGGGCCTA CCGCCTTCCT CGGCTTGGGT GTTGTCGACA ACAACGGCAA 180
140 CGGCGCACGA GTCCAACGCG TGGTCGGGAG CGCTCCGGCG GCAAGTCTCG GCATCTCCAC 240
141 CGGCGACGTG ATCACCGCGG TCGACGGCGC TCCGATCAAC TCGGCCACCG CGATGGCGGA 300
142 CGCGCTTAAC GGGCATCATC CCGGTGACGT CATCTCGGTG AACTGGCAAA CCAAGTCGGG 360
143 CGGCACGCGT ACAGGGAACG TGACATTGGC CGAGGGACCC CCGGCCTGAT TTCGTCGYGG 420
144 ATACCACCCG CCGGCCGGCC AATTGGA 447
146 (2) INFORMATION FOR SEQ ID NO: 5:
148 (i) SEQUENCE CHARACTERISTICS:
149 (A) LENGTH: 604 base pairs
150 (B) TYPE: nucleic acid
151 (C) STRANDEDNESS: single
152 (D) TOPOLOGY: linear
154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
156 GTCCCACTGC GGTCGCCGAG TATGTCGCCC AGCAAATGTC TGGCAGCCGC CCAACGGAAT 60
157 CCGGTGATCC GACGTCGCAG GTTGTCGAAC CCGCCGCCGC GGAAGTATCG GTCCATGCCT 120
158 AGCCCGGCGA CGGCGAGCGC CGGAATGGCG CGAGTGAGGA GGCGGGCAAT TTGGCGGGGC 180
159 CCGGCGACGG NGAGCGCCGG AATGGCGCGA GTGAGGAGGT GGNCAGTCAT GCCCAGNGTG 240
160 ATCCAATCAA CCTGNATTCG GNCTGNNGGN CCATTTGACA ATCGAGGTAG TGAGCGCAAA 300
161 TGAATGATGG AAAACGGGNG GNGACGTCCG NTGTTCTGGT GGTGNTAGGT GNCTGNCTGG 360
162 NGTNGNGGNT ATCAGGATGT TCTTCGNCGA AANCTGATGN CGAGGAACAG GGTGTNCCCG 420
163 NNANNCCNAN GGNGTCCNAN CCCNNNNTCC TCGNCGANAT CANANAGNCG NTTGATGNGA 480
164 NAAAAGGGTG GANCAGNNNN AANTNGNGN CCNAANAANC NNNANNGNNG NNAGNTNGNT 540
165 NNNNTNTTNC ANNNNNNNNTG NNGNNGNCCN NNNCAANCNN NTNNNNGNAA NNGGNTTNTT 600
166 NAAT 604
168 (2) INFORMATION FOR SEQ ID NO: 6:
170 (i) SEQUENCE CHARACTERISTICS:
171 (A) LENGTH: 633 base pairs
172 (B) TYPE: nucleic acid
173 (C) STRANDEDNESS: single
174 (D) TOPOLOGY: linear
176 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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178 TTGCANGTCG AACCACCTCA CTAAAGGGAA CAAAAGCTNG AGCTCCACCG CGGTGGCGGC      60
179 CGCTCTAGAA CTAGTGKATM YYYCKGGCTG CAGSAATYCG GYACGAGCAT TAGGACAGTC      120
180 TAACGGTCCT GTTACGGTGA TCGAATGACC GACGACATCC TGCTGATCGA CACCGACGAA      180
181 CGGGTGCGAA CCCTCACCTT CAACCGGCCG CAGTCCCGYA ACGCGCTCTC GGCGGCGCTA      240
182 CGGGATCGGT TTTTCGCGGY GTTGGYCGAC GCCGAGGYCG ACGACGACAT CGACGTCGTC      300
183 ATCTCACCG GYGCCGATCC GGTGTTCTGC GCCGACTGG ACCTCAAGGT AGCTGGCCGG      360
184 GCAGACCGCG CTGCCGACA TCTACCGCG GTGGGCGGCC ATGACCAAGC CGGTGATCGG      420
185 CGCGATCAAC GGCGCCGCG TCACCGGCG GCTCGAACTG GCGCTGTACT GCGACATCCT      480
186 GATCGCCTCC GAGCACGCC GCTTCGNCGA CACCCACGCC CGGGTGGGGC TGCTGCCAC      540
187 CTGGGGACTC AGTGTGTGCT TGCCGAAAA GGTCGGCATC GGNCTGGGCC GGTGGATGAG      600
188 CCTGACCGGC GACTACCTGT CCGTGACCGA CGC      633

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190 (2) INFORMATION FOR SEQ ID NO: 7:

192 (i) SEQUENCE CHARACTERISTICS:

193 (A) LENGTH: 1362 base pairs

194 (B) TYPE: nucleic acid

195 (C) STRANDEDNESS: single

196 (D) TOPOLOGY: linear

198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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200 CGACGACGAC GGCGCCGAG AGCGGGCGCG AACGGCGATC GACGCGGCC TGGCCAGAGT      60
201 CGGCACCACC CAGGAGGGAG TCGAATCATG AAATTTGTCA ACCATATTGA GCCCGTCGCG      120
202 CCCC GCCGAG CCGGCCGCGC GGTGCGCGAG GTCTATGCCG AGGCCCGCCG CGAGTTCGGC      180
203 CGGCTGCCCG AGCCGCTCGC CATGCTGTCC CCGGACGAGG GACTGCTCAC CGCCGGCTGG      240
204 GCGACGTTGC GCGAGACACT GCTGGTGGGC CAGGTGCCGC GTGGCCGCAA GGAAGCCGTC      300
205 GCCGCCGCCG TCGCGGCCAG CCTGCGCTGC CCCTGGTGCG TCGACGCACA CACCACCATG      360
206 CTGTACGCGG CAGGCCAAAC CGACACCGCC GCGGCGATCT TGGCCGGCAC AGCACCTGCC      420
207 GCCGGTGACC CGAACCGGCC GTATGTGGCG TGGGCGGCAG GAACCGGGAC ACCGGCGGGA      480
208 CCGCCGGCAC CGTTCGGCCC GGATGTCGCC GCCGAATACC TGGGCACCGC GGTGCAATTC      540
209 CACTTCATCG CACGCCTGGT CCTGGTGCTG CTGGACGAAA CCTTCCTGCC GGGGGGCCCC      600
210 CGCGCCCAAC AGCTCATGCG CCGCGCCGGT GGAATGGTGT TCGCCCGCAA GGTGCGCGCG      660
211 GAGCATCGGC CGGGCCGCTC CACCCGCCGG CTCGAGCCGC GAACGCTGCC CGACGATCTG      720
212 GCATGGGCAA CACCGTCCGA GCCCATAGCA ACCGCGTTTC CCGCGCTCAG CCACCACCTG      780
213 GACACCGCGC CGACCTGCC GCCACCGACT CGTCAGGTGG TCAGGCGGGT CGTGGGGTCG      840
214 TGGCACGGCG AGCCAATGCC GATGAGCAGT CGCTGGACGA ACGAGCACAC CGCCGAGCTG      900
215 CCCGCCGACC TGCACGCGCC CACCCGCTTT GCCCTGCTGA CCGGCCTGGC CCCGCATCAG      960
216 GTGACCGACG ACGACGTCGC CGCGGCCCGA TCCCTGCTCG ACACCGATGC GCGCTGGTT      1020
217 GCGCGCCTGG CCTGGGCCGC CTTACCGGCC GCGCGGCGCA TCGGCACCTG GATCGGCGCC      1080
218 GCCGCCGAGG GCCAGGTGTC GCGGCAAAAC CCGACTGGGT GAGTGTGCGC GCCCTGTCGG      1140
219 TAGGGTGTCA TCGCTGGCCC GAGGGATCTC GCGGCGGCGA ACGGAGGTGG CGACACAGGT      1200
220 GGAAGCTGCG CCCACTGGCT TGCGCCCCAA CGCCGTCGTG GCGGTTTCGGT TGGCCGCACT      1260
221 GGCCGATCAG GTCGGCGCCG GCCCTTGGCC GAAGGTCCAG CTCAACGTGC CGTCACCGAA      1320
222 GGACCGGACG GTCACCGGGG GTCACCCTGC GCGCCCAAGG AA      1362

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224 (2) INFORMATION FOR SEQ ID NO: 8:

226 (i) SEQUENCE CHARACTERISTICS:

227 (A) LENGTH: 1458 base pairs

228 (B) TYPE: nucleic acid

229 (C) STRANDEDNESS: single

230 (D) TOPOLOGY: linear

232 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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234 GCGACGACCC CGATATGCCG GGCACCGTAG CGAAAGCCGT CGCCGACGCA CTCGGGCGCG      60

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235 GTATCGCTCC CGTTGAGGAC ATTCAGGACT GCGTGGAGGC CCGGCTGGGG GAAGCCGGTC 120
236 TGGATGACGT GGCCCGTGTT TACATCATCT ACCGGCAGCG GCGCGCCGAG CTGCGGACGG 180
237 CTAAGGCCTT GCTCGGCGTG CGGGACGAGT TAAAGCTGAG CTTGGCGGCC GTGACGGTAC 240
238 TGCGCGAGCG CTATCTGCTG CACGACGAGC AGGGCCGGCC GGCCGAGTCG ACCGGCGAGC 300
239 TGATGGACCG ATCGGCGCGC TGTGTCGCGG CGGCCGAGGA CCAGTATGAG CCGGGCTCGT 360
240 CGAGGCGGTG GGCCGAGCGG TTCGCCACGC TATTACGCAA CCTGGAATTC CTGCCGAATT 420
241 CGCCACGTT GATGAACCTT GGCACCGACC TGGGACTGCT CGCCGGCTGT TTTGTTCTGC 480
242 CGATTGAGGA TTCGCTGCAA TCGATCTTTG CGACGCTGGG ACAGGCCGCC GAGCTGCAGC 540
243 GGGCTGGAGG CGGCACCGGA TATGCGTTCA GCCACCTGCG ACCCGCCGGG GATCGGGTGG 600
244 CCTCCACGGG CGGCACGGCC AGCGGACCGG TGTCGTTTCT ACGGCTGTAT GACAGTGCCG 660
245 CGGGTGTGGT CTCCATGGGC GGTCGCCGGC GTGGCGCCTG TATGGCTGTG CTTGATGTGT 720
246 CGCACCCGGA TATCTGTGAT TTCGTCACCG CCAAGGCCGA ATCCCCAGC GAGCTCCCGC 780
247 ATTTCAACCT ATCGGTTGGT GTGACCGACG CGTTCCTGCG GGCCGTCGAA CGCAACGGCC 840
248 TACACCGGCT GGTCAATCCG CGAACCGGCA AGATCGTCGC GCGGATGCCC GCCGCCGAGC 900
249 TGTTGACGCG CATCTGCAAA GCCGCGCACG CCGGTGGCGA TCCCGGGCTG GTGTTTCTCG 960
250 ACACGATCAA TAGGGCAAAAC CCGGTGCCCG GGAGAGGCCG CATCGAGGCG ACCAACCCGT 1020
251 GCGGGGAGGT CCCACTGCTG CCTTACGAGT CATGTAATCT CGGCTCGATC AACCTCGCCC 1080
252 GGATGCTCGC GCACGGTCGC GTCGACTGGG ACCGGCTCGA GGAGGTCGCC GGTGTGGCGG 1140
253 TGCGGTTTCT TGATGACGTC ATCGATGTCG GCCGCTACCC CTTCCCCGAA CTGGGTGAGG 1200
254 CGGCCCCGCG CACCCGCAAG ATCGGGCTGG GAGTCATGGG TTTGGCGGAA CTGCTTGCCG 1260
255 CACTGGGTAT TCCGTACGAC AGTGAAGAAG CCGTGCGGTT AGCCACCCGG CTCATGCGTC 1320
256 GCATACAGCA GCGGCGGCAC ACGGCATCGC GGAGGCTGGC CGAAGAGCGG GGCGCATTCC 1380
257 CGGCGTTTAC CGATAGCCGG TTCGCGCGGT CGGGCCCCGAG GCGCAACGCA CAGGTCACCT 1440
258 CCGTCGCTCC GACGGGCA 1458

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260 (2) INFORMATION FOR SEQ ID NO: 9:

262 (i) SEQUENCE CHARACTERISTICS:

263 (A) LENGTH: 862 base pairs

264 (B) TYPE: nucleic acid

265 (C) STRANDEDNESS: single

266 (D) TOPOLOGY: linear

268 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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270 ACGGTGTAAT CGTGCTGGAT CTGGAACCGC GTGGCCCGCT ACCTACCGAG ATCTACTGGC 60
271 GGCGCAGGGG GCTGGCCCTG GGCATCGCGG TCGTCGTAGT CCGGATCGCG GTGGCCATCG 120
272 TCATCGCCTT CGTCGACAGC AGCGCCGGT CCAAACCGGT CAGCGCCGAC AAGCCGGCCT 180
273 CCGCCCAGAG CCATCCGGGG TCGCCGCGAC CCAAAGCACC CCAGCCGGCC GGGCAAACCG 240
274 AAGGTAACGC CGCCGCGGCC CCGCCGAGG GCCAAAACCC CGAGACACCC ACGCCCACCG 300
275 CCGCGGTGCA GCCGCCGCCG GTGCTCAAGG AAGGGGACGA TTGCCCCGAT TCGACGCTGG 360
276 CCGTCAAAGG TTTGACCAAC GCGCCGAGT ACTACGTCGG CGACCAGCCG AAGTTCACCA 420
277 TGGTGGTCAC CAACATCGGC CTGGTGTCTT GTAAACGCGA CGTTGGGGCC GCGGTGTTGG 480
278 CCGCCTACGT TTAATCGCTG GACAACAAGC GGTTGTGGTC CAACCTGGAC TGCGCGCCCT 540
279 CGAATGAGAC GCTGGTCAAG ACGTTTTCCT CCGGTGAGCA GGTAACGACC GCGGTGACCT 600
280 GGACCGGGAT GGGATCGGCG CCGCGCTGCC CATTGCCGCG GCCGGCGATC GGGCCGGGCA 660
281 CCTACAATCT CGTGGTACAA CTGGGCAATC TGCGCTCGCT GCCGGTTCCG TTCATCCTGA 720
282 ATCAGCCGCC GCCGCCGCC GGGCCGGTAC CCGCTCCGGG TCCAGCGCAG GCGCCTCCGC 780
283 CGGAGTCTCC CGCGCAAGGC GGATAATTAT TGATCGCTGA TGGTCGATTC CGCCAGCTGT 840
284 GACAACCCCT CGCCTCGTGC CG 862

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286 (2) INFORMATION FOR SEQ ID NO: 10:

288 (i) SEQUENCE CHARACTERISTICS:

289 (A) LENGTH: 622 base pairs

## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10084843.raw

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L:35 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:36 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:1269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54  
L:1325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58  
L:1338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59  
L:1365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61  
L:1415 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63  
L:1481 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65  
L:1535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67  
L:1537 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67  
L:1539 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67  
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L:3755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:131  
L:3772 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:132  
L:3785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:133  
L:3798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:134  
L:3811 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135  
L:3837 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137  
L:4152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:145  
L:4164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:145  
L:10862 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:343  
L:10864 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:343  
L:10879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:344  
L:10894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:345

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L:10909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:346

L:10924 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:347

L:10926 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:347